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MOSSAKOWSKA, Danuta, Ewa, Irena

<120> CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
MEMBRANE-BINDING AGENTS

<130> 37945-0004

<140> US 09/612,314
<141> 2000-07-07

<150> US 09/214,913
<151> 1999-03-16

<150> PCT/EP97/03715
<151> 1997-07-08

<150> GB 96 148 71.3
<151> 1996-07-15

<160> 67

<170> PatentIn Ver. 2.1

<210> 1
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide used to anneal to oligonucleotide
of SEQ ID NO.2

<400> 1
gcaccgcagt gcatcatccc gaacaaatgc taataaaa

37

<210> 2
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide used to anneal to oligonucleotide
of SEQ ID NO.1

<400> 2
atgttttatt agcatttggtt cgggatgtatg cactgcg

37

<210> 3
<211> 85
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide used to anneal to oligonucleotide
of SEQ ID NO.4 to generate fragment 4

<400> 3

gcaccgcagt gcatcatccc gaacaaagac ggtccgaaaa agaagaaaaa gaaatctccg 60
tccaaatctt ccgggttgcta ataaa 85

<210> 4

<211> 85

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide used to anneal to oligonucleotide
of SEQ ID NO.3 to generate fragment 4

<400> 4

agcttttatt agcaaccgga agatggac ggagattct ttttcttc ttccggaccg 60
tcttggttcg ggatgatgca ctgcg 85

<210> 5

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (17)

<223> NH₂ group is linked to the C-terminal cysteine

<220>

<223> Description of Artificial Sequence: Peptide used
to synthesize MSWP-1

<400> 5

Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Pro Gly Asp
1 5 10 15

Cys

<210> 6

<211> 198

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: The peptide
sequence corresponds to short consensus repeats
1-3 of CR1 with a C-terminal cysteine

<400> 6

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys
50						55					60				
Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly
65						70					75			80	
Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg
	85						90					95			
Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val
		100					105				110				
Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu
		115					120				125				
Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn
		130				135				140					
Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly
145					150				155			160			
Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr
		165					170				175				
Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys
					180			185			190				
Ile	Ile	Pro	Asn	Lys	Cys										
		195													

<210> 7
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Short
consensus repeats 1-3 of CR1 with an additional 17
C-terminal amino acids

<400> 7
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val
														110	
Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu
														125	
Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn
														140	
Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly
														160	
Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr
														175	
Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys
														190	
Ile	Ile	Pro	Asn	Lys	Asp	Gly	Pro	Lys	Lys	Lys	Lys	Lys	Ser	Pro	
														205	
Ser	Lys	Ser	Ser	Gly	Cys										
210>	8														
211>	215														
212>	PRT														
213>	Artificial Sequence														
<220>															
<221>	UNSURE														
<222>	(198)..(199)														
<223>	Residues 1-198 are a first polypeptide chain and residues 199-215 are a second polypeptide chain linked by a disulphide bond formed between the cysteines at positions 198 and 199														
<220>															
<221>	UNSURE														
<222>	(215)														
<223>	The C-terminal glycine is linked to an N-(Myristoyl) group														
<220>															
<221>	UNSURE														
<222>	(198)														
<223>	The cysteine at position 198 is -Cys-COOH														
<220>															
<221>	UNSURE														
<222>	(199)														
<223>	The cysteine at position 199 is CONH2-Cys-														
<220>															
<223>	Description of Artificial Sequence:														
<400>	8														
Met	Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn
														15	

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
 20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
 35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
 50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190

Ile Ile Pro Asn Lys Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys
 195 200 205

Ser Pro Ser Lys Ser Ser Gly
 210 215

*disulphide
linked*

<210> 9
 <211> 231
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (214)..(215)
 <223> Residues 1-214 are a first polypeptide chain and residues 215-231 are a second polypeptide chain linked by a disulphide bond formed between the cysteines at positions 214 and 215

<220>
 <221> UNSURE
 <222> (231)
 <223> The C-terminal glycine is linked to an N-[Myristoyl] group

<220>
<223> Description of Artificial Sequence: [SCR1-3/switch
fusion] disulphide linked to [MSWP-1]

<220>
<221> UNSURE
<222> (214)
<223> The cysteine at position 214 is -Cys-COOH

<220>
<221> UNSURE
<222> (215)
<223> The cysteine at position 215 is CONH2-Cys-

<400> 9
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Glu Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180 185 190

Ile Ile Pro Asn Lys Asp Gly Pro Lys Lys Lys Lys Ser Pro
195 200 205

Ser Lys Ser Ser Gly Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys
210 215 220

Ser Pro Ser Lys Ser Ser Gly
225 230

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<210> 10
<211> 1947
<212> PRT
<213> Artificial Sequence

    <220>
    <221> UNSURE
    <222> (1930)..(1931)
    <223> Residues 1-1930 are a first polypeptide chain and
          residues 1931-1947 are a second polypeptide chain
          linked by a disulphide bond formed between the
          cysteines at positions 1930 and 1931

    <220>
    <221> UNSURE
    <222> (1947)
    <223> The C-terminal glycine is linked to an
          N-[Myristoyl] group

    <220>
    <223> Description of Artificial Sequence: [CR1: 1-1929]
          - Cys-S-S-[MSWP-1]

    <220>
    <221> UNSURE
    <222> (1930)
    <223> The cysteine at position 1930 is -Cys-COOH

    <220>
    <221> UNSURE
    <222> (1931)
    <223> The Cysteine at position 1931 is CONH2-Cys-

<400> 10
Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
      1           5           10          15

Thr Asp Glu Phe Glu Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
      20          25           30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
      35          40           45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
      50          55           60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
      65          70           75           80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
      85          90           95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
      100         105          110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
      115         120          125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
      130         135          140

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His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
 145 150 155 160
 Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
 165 170 175
 Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
 180 185 190
 Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 195 200 205
 Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 210 215 220
 Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240
 Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255
 Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270
 Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285
 Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300
 Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320
 Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335
 Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350
 Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365
 Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380
 Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400
 Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415
 Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430
 Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445
 Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
500 505 510

Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr
515 520 525

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile
645 650 655

Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu
660 665 670

Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys
675 680 685

Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
690 695 700

Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
705 710 715 720

Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
725 730 735

Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
740 745 750

Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
755 760 765

Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
770 775 780

Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln
 785 790 795 800

 Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
 805 810 815

 Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
 820 825 830

 Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
 835 840 845

 Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
 850 855 860

 Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
 865 870 875 880

 Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
 885 890 895

 Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
 900 905 910

 Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
 915 920 925

 Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
 930 935 940

 Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
 945 950 955 960

 Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
 965 970 975

 Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
 980 985 990

 Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
 995 1000 1005

 Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro
 1010 1015 1020

 Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn
 1025 1030 1035 1040

 Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Leu
 1045 1050 1055

 Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
 1060 1065 1070

 Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala
 1075 1080 1085

 Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn
 1090 1095 1100

Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val
1105 1110 1115 1120

Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg
1125 1130 1135

Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys
1140 1145 1150

Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu His Gly Glu His Thr
1155 1160 1165

Pro Ser His Gln Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser
1170 1175 1180

Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Leu His Cys Thr
1185 1190 1195 1200

Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg Cys Ala Val Lys Ser
1205 1210 1215

Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu Phe Pro
1220 1225 1230

Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe Val Cys Asp Glu Gly
1235 1240 1245

Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val Gly Met
1250 1255 1260

Arg Ser Leu Trp Asn Asn Ser Val Pro Val Cys Glu His Ile Phe Cys
1265 1270 1275 1280

Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His Thr Gly Thr Pro Ser
1285 1290 1295

Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp Pro His
1300 1305 1310

Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr Ile Arg
1315 1320 1325

Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro Ala Pro
1330 1335 1340

Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro Glu Gln
1345 1350 1355 1360

Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu Phe Pro
1365 1370 1375

Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe Gly Lys
1380 1385 1390

Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser Val Glu
1395 1400 1405

Asp Asn Cys Arg Arg Lys Ser Cys Gly Pro Pro Pro Glu Pro Phe Asn
1410 1415 1420

Gly Met Val His Ile Asn Thr Asp Thr Gln Phe Gly Ser Thr Val Asn
 1425 1430 1435 1440
 Tyr Ser Cys Asn Glu Gly Phe Arg Leu Ile Gly Ser Pro Ser Thr Thr
 1445 1450 1455
 Cys Leu Val Ser Gly Asn Asn Val Thr Trp Asp Lys Lys Ala Pro Ile
 1460 1465 1470
 Cys Glu Ile Ile Ser Cys Glu Pro Pro Pro Thr Ile Ser Asn Gly Asp
 1475 1480 1485
 Phe Tyr Ser Asn Asn Arg Thr Ser Phe His Asn Gly Thr Val Val Thr
 1490 1495 1500
 Tyr Gln Cys His Thr Gly Pro Asp Gly Glu Gln Leu Phe Glu Leu Val
 1505 1510 1515 1520
 Gly Glu Arg Ser Ile Tyr Cys Thr Ser Lys Asp Asp Gln Val Gly Val
 1525 1530 1535
 Trp Ser Ser Pro Pro Arg Cys Ile Ser Thr Asn Lys Cys Thr Ala
 1540 1545 1550
 Pro Glu Val Glu Asn Ala Ile Arg Val Pro Gly Asn Arg Ser Phe Phe
 1555 1560 1565
 Ser Leu Thr Glu Ile Ile Arg Phe Arg Cys Gln Pro Gly Phe Val Met
 1570 1575 1580
 Val Gly Ser His Thr Val Gln Cys Gln Thr Asn Gly Arg Trp Gly Pro
 1585 1590 1595 1600
 Lys Leu Pro His Cys Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu
 1605 1610 1615
 His Gly Glu His Thr Leu Ser His Gln Asp Asn Phe Ser Pro Gly Gln
 1620 1625 1630
 Glu Val Phe Tyr Ser Cys Glu Pro Ser Tyr Asp Leu Arg Gly Ala Ala
 1635 1640 1645
 Ser Leu His Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg
 1650 1655 1660
 Cys Thr Val Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly
 1665 1670 1675 1680
 Arg Val Leu Leu Pro Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe
 1685 1690 1695
 Val Cys Asp Glu Gly Phe Arg Leu Lys Gly Arg Ser Ala Ser His Cys
 1700 1705 1710
 Val Leu Ala Gly Met Lys Ala Leu Trp Asn Ser Ser Val Pro Val Cys
 1715 1720 1725
 Glu Gln Ile Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His
 1730 1735 1740

Thr Gly Thr Pro Phe Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr
 1745 1750 1755 1760

 Ala Cys Asp Thr His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly
 1765 1770 1775

 Glu Ser Ser Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp
 1780 1785 1790

 Ser Ser Pro Ala Pro Arg Cys Glu Leu Ser Val Pro Ala Ala Cys Pro
 1795 1800 1805

 His Pro Pro Lys Ile Gln Asn Gly His Tyr Ile Gly Gly His Val Ser
 1810 1815 1820

 Leu Tyr Leu Pro Gly Met Thr Ile Ser Tyr Thr Cys Asp Pro Gly Tyr
 1825 1830 1835 1840

 Leu Leu Val Gly Lys Gly Phe Ile Phe Cys Thr Asp Gln Gly Ile Trp
 1845 1850 1855

 Ser Gln Leu Asp His Tyr Cys Lys Glu Val Asn Cys Ser Phe Pro Leu
 1860 1865 1870

 Phe Met Asn Gly Ile Ser Lys Glu Leu Glu Met Lys Lys Val Tyr His
 1875 1880 1885

 Tyr Gly Asp Tyr Val Thr Leu Lys Cys Glu Asp Gly Tyr Thr Leu Glu
 1890 1895 1900

 Gly Ser Pro Trp Ser Gln Cys Gln Ala Asp Asp Arg Trp Asp Pro Pro
 1905 1910 1915 1920

 Leu Ala Lys Cys Thr Ser Arg Ala His Cys Cys Asp Gly Pro Lys Lys
 1925 1930 1935

 Lys Lys Lys Ser Pro Ser Lys Ser Ser Gly
 1940 1945

<210> 11
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (198)..(199)
 <223> Residues 1-198 are a first polypeptide chain and
 residues 199-215 are a second polypeptide chain
 linked by a disulphide bond formed between the
 cysteines at positions 198 and 199

<220>
 <221> UNSURE
 <222> (199)
 <223> The cysteine at position 199 is linked to a
 NHCOCH₃ group

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<220>
<221> UNSURE
<222> (215)
<223> The C-terminal lysine is linked to an
      N-[Myristoyl]-NH2 group

<220>
<223> Description of Artificial Sequence:
      [SCR1-3]-Cys-S-S-[MSWP-2]

<400> 11
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
    1           5           10          15

Leu Thr Asp Glu Phe Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
    20          25          30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
    35          40          45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
    50          55          60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
    65          70          75          80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
    85          90          95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
    100         105         110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
    115         120         125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
    130         135         140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
    145         150         155         160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
    165         170         175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
    180         185         190

Ile Ile Pro Asn Lys Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys
    195         200         205

Ser Pro Ser Lys Ser Ser Lys
    210         215

<210> 12
<211> 213
<212> PRT
<213> Artificial Sequence

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<220>
 <221> UNSURE
 <222> (198)...(199)
 <223> Residues 1-198 are a first polypeptide chain and residues 199-213 are a second polypeptide chain linked by a disulphide bond formed between the cysteines at positions 198 and 199

<220>
 <221> UNSURE
 <222> (199)
 <223> The cysteine at position 199 is linked to a CONH₂ group

<220>
 <221> UNSURE
 <222> (213)
 <223> The C-terminal serine is linked to an NH-[Myristoyl] group

<220>
 <223> Description of Artificial Sequence:
 [SCR1-3]-Cys-S-S-[MSWP-3]

<400> 12
 Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
 1 5 10 15

Leu Thr Asp Glu Phe Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
 20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
 35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
 50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190

Ile Ile Pro Asn Lys Cys Cys Lys Thr Lys Ser Lys Lys Lys Lys Lys
 195 200 205

Lys Gly Asp Lys Ser
 210

<210> 13
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (198)..(199)
<223> Residues 1-198 are a first polypeptide chain and residues 199-214 are a second polypeptide chain linked by a disulphide bond formed between the cysteines at positions 198 and 199

<220>
<221> UNSURE
<222> (199)
<223> The cysteine at position 199 is linked to an NHCOCH₃ group

<220>
<221> UNSURE
<222> (214)
<223> The C-terminal valine is linked to an -NH(CH₂)₉CH₃ group.

<220>
<223> Description of Artificial Sequence:
[SCR1-3]-Cys-S-S-[TCPT-1]

<400> 13
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
 1 5 10 15

Leu Thr Asp Glu Phe Glu Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
 20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
 35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
 50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180 185 190

Ile Ile Pro Asn Lys Cys Cys Ser Ala Ala Pro Ser Ser Gly Phe Arg
195 200 205

Ile Leu Leu Leu Lys Val
210

<210> 14

<211> 209

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SCR1-3 with
the C-terminal amino acids N195 and K196 replaced
by a 14 amino acid peptide.

<400> 14

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Glu Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180 185 190

Ile Ile Pro Thr Asn Ala Asn Lys Ser Leu Ser Ser Ile Ser Cys Gln
195 200 205

Thr

<210> 15

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide used to generate a novel
restriction site and a C-terminal cysteine in
plasmid pBC04-29

<400> 15

ctggagcggg cccgcaccgc agtgcatcat cccgaacaaa tgctaataaa agc

53

<210> 16

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide used to generate a novel
restriction site and C-terminal cysteine residue
in plasmid pBC04-29

<400> 16

gcttttattta gcatttgttc gggatgatgc actgcgggtgc gggcccgctc cag

53

<210> 17

<211> 224

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (1)..(209)

<223> Positions 1-209 are a first polypeptide chain
which is linked to a second polypeptide chain
(positions 210-224) by a disulphide linkage
between the cysteines at positions 207 and 210.

<220>

<221> UNSURE

<222> (210)

<223> The cysteine at position 210 is linked to a -CONH₂
group

<220>
 <221> UNSURE
 <222> (224)
 <223> The glycine at position 224 is linked to an
 -NH-[Myristoyl] group

<220>
 <223> Description of Artificial Sequence:
 [SCR1-3 (delN195-K196)]TNANKSLSSISC-(-S-S-[MSWP-1])
 QT

<400> 17
 Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
 1 5 10 15

Leu Thr Asp Glu Phe Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
 20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
 35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
 50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190

- Ile Ile Pro Thr Asn Ala Asn Lys Ser Leu Ser Ser Ile Ser Cys Gln
 195 200 205

.Thr Cys Asp Gly Pro Lys Lys Lys Lys Ser Lys Ser Ser Gly
 210 215 220

<210> 18
 <211> 17
 <212> PRT
 <213> Artificial Sequence

```

<220>
<221> UNSURE
<222> (17)
<223> The C-terminal lysine is linked to an -NH2 group

<220>
<223> Description of Artificial Sequence: Peptide used
      to generate SEQ ID NO.28

<400> 18
Cys Asp Gly Pro Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser
    1           5           10          15

Lys

<210> 19
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide used
      to generate SEQ ID NO.29

<400> 19
Ser Lys Asp Gly Lys Lys Lys Lys Lys Ser Lys Thr Lys Cys
    1           5           10          15

<210> 20
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide used
      to generate SEQ ID NO.30

<400> 20
Cys Ser Ala Ala Pro Ser Ser Gly Phe Arg Ile Leu Leu Leu Lys Val
    1           5           10          15

<210> 21
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (1)
<223> The N-terminal glycine is linked to an
      N-[Myristoyl]- group

<220>
<221> UNSURE
<222> (17)
<223> The C-terminal cysteine is linked to
      -S-S-[4-butyrimino]-N-epsilon(Lys) [Streptokinase]

```

<220>
 <221> UNSURE
 <222> (17)
 - <223> The C-terminal cysteine is linked to an -NH₂ group

<220>
 <223> Description of Artificial Sequence: Conjugate of Streptokinase and MSWP-1

<400> 21
 Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Pro Gly Asp
 1 5 10 15

Cys

<210> 22
 <211> 527
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (478)
 <223> Serine 478 is modified to:
 O-4-CO-benzyl-NH(CH₂)₂NHCO(CH₂)₂-S-S-{Cys (-CONH₂) - Asp-Gly-Pro-Lys-Lys-Lys-Lys-Ser-Pro-Ser-Lys-Ser-Ser-Gly} --NH- [Myristoyl]

<220>
 <223> Description of Artificial Sequence: Reversible linkage of MSWP-1 to the active centre of Human Tissue-type Plasminogen Activator

<400> 22
 Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln
 1 5 10 15

Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
 20 25 30

Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val
 35 40 45

Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
 50 55 60

Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
 65 70 80

Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln
 85 90 95

Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu
 100 105 110

Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly
 115 120 125

Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys
 130 135 140
 Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala
 145 150 155 160
 Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly
 165 170 175
 Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His
 180 185 190
 Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile
 195 200 205
 Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu
 210 215 220
 Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys
 225 230 235 240
 Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys
 245 250 255
 Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro
 260 265 270
 Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro
 275 280 285
 Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro Gly Glu Arg
 290 295 300
 Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala
 305 310 315 320
 Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile
 325 330 335
 Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe
 340 345 350
 Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr
 355 360 365
 Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys
 370 375 380
 Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp
 385 390 395 400
 Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys
 405 410 415
 His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys Glu Ala His
 420 425 430
 Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
 435 440 445

Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly
450 455 460

Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly
465 470 475 480

Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile
485 490 495

Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr
500 505 510

Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met Arg Pro
515 520 525

<210> 23

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SCR1-3 with an
additional 14 amino acid residues at the
C-terminus

<400> 23

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110

- Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125

. Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180 185 190

Ile Ile Pro Asn Lys Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe
195 200 205

Ser Ser Cys
210

<210> 24
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (211)...(212)
<223> Residues 1-211 are a first polypeptide chain and residues 212-228 are a second polypeptide chain linked by a disulphide bond formed between the cysteines at positions 211 and 212

<220>
<221> UNSURE
<222> (228)
<223> The C-terminal glycine is linked to an -NH-[Myristoyl] group

<220>
<223> Description of Artificial Sequence: SCR1-3 with an additional C-terminal 14 amino acid residues reacted with MSWP-1

<400> 24
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180 185 190

Ile Ile Pro Asn Lys Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe
195 200 205

Ser Ser Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Ser Pro Ser
210 215 220

Lys Ser Ser Gly
225

<210> 25
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide used with the oligonucleotide of
SEQ ID NO. 26 and plasmid pBC04-29 to generate
pBC04-31

<400> 25
cgcacccgcaag tgcatcatcc cgaacaaaga tggcccgagc gaaattctgc gtggcgattt 60
tagcagctgc ta 72

<210> 26
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide used with oligonucleotide of SEQ
ID NO. 25 and plasmid pBC04-29 to generate plasmid
pBC04-31

<400> 26
acgttagcag ctgctaaaat cgccacgcag aatttcgctc gggccatctt tgttcggat 60
- gatgcactgc ggtgcgggcc 80

<210> 27
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (1)
<223> The N-terminal glycine is linked to an
N-[Myristoyl]- group

```

<220>
<223> Description of Artificial Sequence:
      Myristoyl/Electrostatic Switch Peptide Reagent 1
      (MSWP-1)

<220>
<221> UNSURE
<222> (17)
<223> The cysteine at position 17 is (S-
      2-Thiopyridyl)Cys-NH2

<400> 27
Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Pro Gly Asp
    1           5           10          15

Cys

<210> 28
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (1)
<223> The N-terminal Cys is
      N-acetyl-(S-2-thiopyridyl)Cys-

<220>
<221> UNSURE
<222> (17)
<223> The C-terminal lysine is
      -(epsilonN-(Myristoyl))Lys-NH2

<220>
<223> Description of Artificial Sequence:
      Myristoyl/Electrostatic Switch Peptide Reagent 2
      (MSWP-2)

<400> 28
Cys Asp Gly Pro Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser
    1           5           10          15

Lys

<210> 29
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (1)
<223> The N-terminal serine is N-(Myristoyl)-Ser-

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<220>
<221> UNSURE
<222> (15)
<223> The C-terminal cysteine is
      - (S-2-Thiopyrody1)Cys-NH2

<220>
<223> Description of Artificial Sequence:
      Myristoyl/Electrostatic Switch Peptide Reagent 3
      (MSWP-3)

<400> 29
Ser Lys Asp Gly Lys Lys Lys Lys Lys Ser Lys Thr Lys Cys
    1           5           10          15

<210> 30
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (1)
<223> The N-terminal cysteine is
      N-acetyl-(S-2-thiopyridyl)Cys-

<220>
<221> UNSURE
<222> (16)
<223> The C-terminal valine is -Val-NH(CH2)9CH3

<220>
<223> Description of Artificial Sequence: T-cell
      targetting peptide reagent 1 (TCTP-1)

<400> 30
Cys Ser Ala Ala Pro Ser Ser Gly Phe Arg Ile Leu Leu Leu Lys Val
    1           5           10          15

<210> 31
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (214)
<223> The C-terminal cysteine is
      -Cys-S-S-(CH2)2-CONH-(CH2)12CH3

<220>
<223> Description of Artificial Sequence: [SCR1-3/switch
      fusion]disulphide linked to [MAET]

<400> 31
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
    1           5           10          15

```

Leu Thr Asp Glu Phe Glu Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
 20 25 30

 Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
 35 40 45

 Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
 50 55 60

 Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80

 Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95

 Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110

 Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125

 Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140

 Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160

 Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175

 Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190

 Ile Ile Pro Asn Lys Asp Gly Pro Lys Lys Lys Lys Lys Ser Pro
 195 200 205

 Ser Lys Ser Ser Gly Cys
 210

<210> 32
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (1)
 - <223> The N-terminal Glycine is N-(Myristoyl)-Gly-

<220>
 - <221> UNSURE
 <222> (17)
 <223> The C-terminal cysteine is linked to an amino group and is also linked via a disulphide bond to -[4-butyrimino]-N-epsilon(Lys) [Rabbit anti-(human erythrocyte membrane)] antibody].

<220>
 <223> Description of Artificial Sequence: Rabbit anti-(human erythrocyte membrane)

antibody-[MSWP-1] conjugate.

<400> 32

Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Pro Gly Asp
1 5 10 15

Cys

<210> 33

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SCR1-3 with an
additional C-terminal 18 amino acids

<400> 33

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180 185 190

Ile Ile Pro Asn Lys Ala Ala Pro Ser Val Ile Gly Phe Arg Ile Leu
195 200 205

Leu Leu Lys Val Gly Cys
210

```

<210> 34
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide used with oligonucleotide of SEQ
      ID NO.35 and plasmid pBC04-29 to generate plasmid
      pBC04-34

<400> 34
cgcacccgcaag tgcatcatcc cgaacaaagc ggcgcccagc gtgattggct tccgtattct 60
gctgctgaaa gtggcggtt gcta                                84

<210> 35
<211> 92
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide used with the oligonucleotide of
      SEQ ID NO. 34 and plasmid pBC04-29 to generate
      plasmid pBC04-34

<400> 35
agcttagcag cccgccactt tcagcagcag aatacggaaag ccaatcacgc tgggcgcgc 60
tttgttcggg atgatgcact gcgggtgcggg cc                                92

<210> 36
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (214)..(215)
<223> Residues 1-214 are a first polypeptide chain and
      residues 215-231 are a second polypeptide chain
      linked by a disulphide bond formed between the
      cysteines at positions 214 and 215

<220>
<221> UNSURE
<222> (231)
<223> The C-terminal glycine is -Gly-NH-[Myristoyl]

<220>
<223> Description of Artificial Sequence: [SCR1-3] with
      an additional 18 C-terminal amino acid residues
      linked via a disulphide bond to MSWP-1

<400> 36
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
    1           5           10          15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
    20          25          30

```

Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys
35							40						45		
Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys
50							55					60			
Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly
65						70				75			80		
Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg
				85					90				95		
Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val
			100					105					110		
Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu
	115					120					125				
Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn
	130					135					140				
Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly
145					150				155			160			
Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr
				165				170				175			
Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys
				180				185				190			
Ile	Ile	Pro	Asn	Lys	Ala	Ala	Pro	Ser	Val	Ile	Gly	Phe	Arg	Ile	Leu
				195				200				205			
Leu	Leu	Lys	Val	Gly	Cys	Cys	Asp	Gly	Pro	Lys	Lys	Lys	Lys	Lys	Lys
			210			215				220					
Ser	Pro	Ser	Lys	Ser	Ser	Gly									
	225			230											

<210> 37

<211> 77

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Protein APT631

<400> 37

Leu	Gln	Cys	Tyr	Asn	Cys	Pro	Asn	Pro	Thr	Ala	Asp	Cys	Lys	Thr	Ala
1					5				10				15		

Val	Asn	Cys	Ser	Ser	Asp	Phe	Asp	Ala	Cys	Leu	Ile	Thr	Lys	Ala	Gly
				20				25					30		

Leu	Gln	Val	Tyr	Asn	Lys	Cys	Trp	Lys	Phe	Glu	His	Cys	Asn	Phe	Asn
				35				40				45			

Asp	Val	Thr	Thr	Arg	Leu	Arg	Glu	Asn	Glu	Leu	Thr	Tyr	Tyr	Cys	Cys
				50				55				60			

Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn
65 70 75

<210> 38
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (1)
<223> The N-terminal glycine is linked to an
N-[Myristoyl]- group

<220>
<221> UNSURE
<222> (17)
<223> The C-terminal cysteine is linked to
-2-thiopyridyl

<220>
<221> UNSURE
<222> (17)
<223> The C-terminal cysteine is linked to an -NH₂ group

<220>

<223> Description of Artificial Sequence: Protein APT542

<400> 38
Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Pro Gly Asp
1 5 10 15

Cys

<210> 39
<211> 70
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protein APT634

<400> 39
Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala
1 5 10 15

Val Ala Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
20 25 30

Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
35 40 45

Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
50 55 60

Lys Lys Asp Leu Cys Asn
65 70

<210> 40
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protein APT2060

<400> 40
Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala
1 5 10 15

Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
20 25 30

Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
35 40 45

Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
50 55 60

Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Gly Gly Thr
65 70 75 80

Ser Cys

<210> 41
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protein APT635

<400> 41
Met Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr
1 5 10 15

Ala Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala
20 25 30

Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe
35 40 45

Asn Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys
50 55 60

Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Gly Gly
65 70 75 80

Thr Ser Cys

<210> 42
<211> 71
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protein APT2061

<400> 42
Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala
1 5 10 15

Val Ala Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
20 25 30

Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
35 40 45

Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
50 55 60

Lys Lys Asp Leu Cys Asn Cys
65 70

<210> 43
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (82)...(83)
<223> Residues 1-82 are a first polypeptide chain and
residues 83-99 are a second polypeptide chain
linked by a disulphide bond formed between the
cysteines at positions 82 and 83

<220>
<221> UNSURE
<222> (99)
<223> The C-terminal glycine is linked to an
NH-[Myristoyl] group

<220>
<223> Description of Artificial Sequence: Protein APT2062

<400> 43
Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala
1 5 10 15

Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
20 25 30

Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
35 40 45

Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
50 55 60

Lys	Lys	Asp	Leu	Cys	Asn	Phe	Asn	Glu	Gln	Leu	Glu	Asn	Gly	Gly	Thr
65															80
Ser	Cys	Cys	Asp	Gly	Pro	Lys	Lys	Lys	Lys	Lys	Ser	Pro	Ser	Lys	
															95
Ser Ser Gly															

<210>	44														
<211>	100														
<212>	PRT														
<213>	Artificial Sequence														
<220>															
<221>	UNSURE														
<222>	(83)..(84)														
<223>	Residues 1-83 are a first polypeptide chain and residues 84-100 are a second polypeptide chain linked by a disulphide bond formed between the cysteines at positions 83 and 84														
<220>															
<221>	UNSURE														
<222>	(100)														
<223>	The C-terminal glycine is linked to an NH-[Myristoyl] group														
<220>															
<223>	Description of Artificial Sequence: Protein APT2063														
<400>	44														
Met	Leu	Gln	Cys	Tyr	Asn	Cys	Pro	Asn	Pro	Thr	Ala	Asp	Cys	Lys	Thr
1															15
Ala	Val	Asn	Cys	Ser	Ser	Asp	Phe	Asp	Ala	Cys	Leu	Ile	Thr	Lys	Ala
															30
Gly	Leu	Gln	Val	Tyr	Asn	Lys	Cys	Trp	Lys	Phe	Glu	His	Cys	Asn	Phe
															45
Asn	Asp	Val	Thr	Thr	Arg	Leu	Arg	Glu	Asn	Glu	Leu	Thr	Tyr	Tyr	Cys
															50
Cys	Lys	Lys	Asp	Leu	Cys	Asn	Phe	Asn	Glu	Gln	Leu	Glu	Asn	Gly	Gly
															60
-	Thr	Ser	Cys	Cys	Asp	Gly	Pro	Lys	Lys	Lys	Lys	Ser	Pro	Ser	
															85
-	Lys	Ser	Ser	Gly											90
															95
Lys Ser Ser Gly															
															100
<210>	45														
<211>	88														
<212>	PRT														
<213>	Artificial Sequence														

<220>
<221> UNSURE
<222> (71)..(72)
<223> Residues 1-71 are a first polypeptide chain and residues 72-88 are a second polypeptide chain linked by a disulphide bond formed between the cysteines at positions 71 and 72

<220>
<221> UNSURE
<222> (88)
<223> The C-terminal glycine is linked to an NH-[Myristoyl] group

<220>
<223> Description of Artificial Sequence: Protein APT2065

<400> 45
Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala
1 5 10 15

Val Ala Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
20 25 30

Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
35 40 45

Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
50 55 60

Lys Lys Asp Leu Cys Asn Cys Cys Asp Gly Pro Lys Lys Lys Lys
65 70 75 80

Lys Ser Pro Ser Lys Ser Ser Gly
85

<210> 46
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protein APT2057

<400> 46
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

Arg Gly Ser His Met Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala
20 25 30

Ser Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr
35 40 45

Val Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu
50 55 60

Ser Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val
65 70 75 80

Glu Phe Cys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn
 85 90 95
 Gly Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser
 100 105 110
 Phe Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe
 115 120 125
 Cys Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu
 130 135 140
 Cys Arg Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile
 145 150 155 160
 Ile Gln Gly Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr
 165 170 175
 Ala Cys Asn Lys Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys
 180 185 190
 Thr Val Asn Asn Asp Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys
 195 200 205
 Arg Gly Cys
 210

<210> 47
 <211> 274
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Protein APT2058

 <400> 47
 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15

 Arg Gly Ser His Met Gln Asp Cys Gly Leu Pro Pro Asp Val Pro Asn
 20 25 30

 Ala Gln Pro Ala Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val
 35 40 45

 Ile Thr Tyr Lys Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys
 50 55 60

 Asp Ser Val Ile Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu
 65 70 75 80

 Phe Cys Asn Arg Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser
 85 90 95

 Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val
 100 105 110

 Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser
 115 120 125

Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu
 130 135 140
 Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly
 145 150 155 160
 Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe
 165 170 175
 Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys
 180 185 190
 Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys
 195 200 205
 Arg Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile
 210 215 220
 Gln Gly Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala
 225 230 235 240
 Cys Asn Lys Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr
 245 250 255
 Val Asn Asn Asp Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg
 260 265 270
 Gly Cys

<210> 48
 <211> 291
 <212> PRT
 <213> Artificial Sequence

 <220>
 <221> UNSURE
 <222> (274)..(275)
 <223> Residues 1-274 are a first polypeptide chain and
 residues 275-291 are a second polypeptide chain
 linked by a disulphide bond formed between the
 cysteines at positions 274 and 275

 <220>
 <221> UNSURE
 <222> (291)
 <223> The C-terminal glycine is linked to an
 NH-[Myristoyl] group

 <220>
 <223> Description of Artificial Sequence: Protein APT2160

 <400> 48
 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15
 Arg Gly Ser His Met Gln Asp Cys Gly Leu Pro Pro Asp Val Pro Asn
 20 25 30

Ala Gln Pro Ala Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val
 35 40 45

 Ile Thr Tyr Lys Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys
 50 55 60

 Asp Ser Val Ile Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu
 65 70 75 80

 Phe Cys Asn Arg Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser
 85 90 95

 Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val
 100 105 110

 Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser
 115 120 125

 Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu
 130 135 140

 Phe Cys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly
 145 150 155 160

 Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe
 165 170 175

 Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys
 180 185 190

 Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys
 195 200 205

 Arg Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile
 210 215 220

 Gln Gly Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala
 225 230 235 240

 Cys Asn Lys Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr
 245 250 255

 Val Asn Asn Asp Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg
 260 265 270

 Gly Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Ser Pro Ser Lys
 275 280 285

- Ser Ser Gly
 290

<210> 49
 <211> 228
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (211)...(212)
 <223> Residues 1-211 are a first polypeptide chain and

residues 212-228 are a second polypeptide chain linked by a disulphide bond formed between the cysteines at positions 211 and 212

<220>

<221> UNSURE

<222> (228)

<223> The C-terminal glycine is linked to an NH- [Myristoyl] group

<220>

<223> Description of Artificial Sequence: Protein APT2184

<400> 49

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

Arg Gly Ser His Met Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala
20 25 30

Ser Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr
35 40 45

Val Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu
50 55 60

Ser Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val
65 70 75 80

Glu Phe Cys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn
85 90 95

Gly Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser
100 105 110

Phe Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe
115 120 125

Cys Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu
130 135 140

Cys Arg Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile
145 150 155 160

Ile Gln Gly Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr
165 170 175

Ala Cys Asn Lys Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys
180 185 190

Thr Val Asn Asn Asp Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys
195 200 205

Arg Gly Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Ser Pro Ser
210 215 220

Lys Ser Ser Gly
225

<210> 50

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 50

Asp Gly Pro Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser Gly
1 5 10 15

<210> 51

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 51

Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Pro Gly Asp
1 5 10 15

<210> 52

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 52

Ser Pro Ser Asn Glu Thr Pro Lys Lys Lys Lys Arg Phe Ser Phe
1 5 10 15

Lys Lys Ser Gly
20

<210> 53

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 53

Asp Gly Pro Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser Lys
1 5 10 15

<210> 54

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 54

Ser Lys Asp Gly Lys Lys Lys Lys Lys Ser Lys Thr Lys
1 5 10

<210> 55

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 55

Gly Arg Gly Asp Ser Pro
1 5

<210> 56

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 56

Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe Ser Ser
1 5 10

<210> 57

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 57

Gly Asn Glu Gln Ser Phe Arg Val Asp Leu Arg Thr Leu Leu Arg Tyr
1 5 10 15

Ala

<210> 58

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 58

Gly Phe Arg Ile Leu Leu Leu Lys Val
1 5

<210> 59

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 59

Ser Ala Ala Pro Ser Ser Gly Phe Arg Ile Leu Leu Leu Lys Val
1 5 10 15

<210> 60

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 60

Ala Ala Pro Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
1 5 10 15

Gly

<210> 61

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 61

Asp Gly Pro Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser Gly
1 5 10 15

Cys

<210> 62

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

-> <223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 62

Ala Ala Pro Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
1 5 10 15

Gly Cys

<210> 63

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

-> <223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 63

Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe Ser Ser Cys
1 5 10

<210> 64

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

-> <223> Description of Artificial Sequence: illustrative DNA oligonucleotide

<400> 64

cctctggcca aatgtacctc tcgtgcacat tgctga

36

<210> 65

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

-> <223> Description of Artificial Sequence: Amino acid leader sequence

<400> 65

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

Arg Gly Ser His
20

<210> 66
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer DAF-R

<400> 66
ggaattctaa gtcagcaagc ccatggttac t

31

<210> 67
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide
DAF-F

<400> 67
gcatatgacc gtcgcgcggc cgagc

25